

SEQUENCE LISTING

<110> CINES, Douglas B
HIGAZI, Abd Al-Roof

<120> COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
TISSUE CONTRACTABILITY

<130> 9596-331

<140>

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<150> US 60/212,847

<151> 2000-06-20

<160> 18

<170> PatentIn Ver. 2.1

<210> 1

<211> 88

<212> PRT

<213> Homo sapiens

<400> 1

Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser
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Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val
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Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly
35 40 45

Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro
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Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met
65 70 75 80

Val His Asp Cys Ala Asp Gly Lys
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<212> PRT

<213> Homo sapiens

<400> 2

Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
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Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
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Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser
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<210> 3

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<213> Homo sapiens

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Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
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Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
20 25 30

Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
35 40 45

Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
50 55 60

Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65 70 75 80

Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
85 90 95

Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
100 105 110

Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
115 120 125

His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
130 135 140

Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145 150 155 160

Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile
165 170 175

Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
180 185 190

Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
195 200 205

Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
210 215 220

Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile
225 230 235 240

Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
245 250 255

Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
260 265 270

Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
275 280 285

Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
290 295 300

Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305 310 315 320

Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
325 330 335

Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
340 345 350

Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
355 360 365

Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
370 375 380

Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385 390 395 400

Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
405 410

<210> 4
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Gly	Thr	Cys	Val	Ser	Asn	Lys	Tyr	Phe	Ser	Asn	Ile	His	Trp	Cys	Asn
			20					25					30		
Cys	Pro	Lys	Lys	Phe	Gly	Gly	Gln	His	Cys	Glu	Ile	Asp	Lys	Ser	Lys
		35					40					45			
Thr	Cys	Tyr	Glu	Gly	Asn	Gly	His	Phe	Tyr	Arg	Gly	Lys	Ala	Ser	Thr
	50					55					60				
Asp	Thr	Met	Gly	Arg	Pro	Cys	Leu	Pro	Trp	Asn	Ser	Ala	Thr	Val	Leu
65					70					75					80
Gln	Gln	Thr	Tyr	His	Ala	His	Arg	Ser	Asp	Ala	Leu	Gln	Leu	Gly	Leu
				85					90					95	
Gly	Lys	His	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Asn	Arg	Arg	Arg	Pro	Trp
		100						105					110		
Cys	Tyr	Val	Gln	Val	Gly	Leu	Lys	Pro	Leu	Val	Gln	Glu	Cys	Met	Val
		115					120					125			
His	Asp	Cys	Ala	Asp	Gly	Lys									
	130					135									

<210> 5
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 <213> Homo sapiens

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Thr	Leu	Arg	Pro	Arg	Phe	Lys	Ile	Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile
		20						25					30		

Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly
 35 40 45
 Ser Val Thr Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val
 50 55 60
 Ile Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr
 65 70 75 80
 Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu
 85 90 95
 Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala
 100 105 110
 Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser
 115 120 125
 Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys
 130 135 140
 Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile
 145 150 155 160
 Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln
 165 170 175
 Leu Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln
 180 185 190
 Pro His Tyr Tyr Gly Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala
 195 200 205
 Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
 210 215 220
 Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser
 225 230 235 240
 Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg
 245 250 255
 Val Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn
 260 265 270
 Gly Leu Ala Leu
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<210> 6
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<400> 6
 Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
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 Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
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 Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
 35 40 45
 Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
 50 55 60
 Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
 65 70 75 80
 Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
 85 90 95
 Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
 100 105 110
 Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
 115 120 125
 His Asp Cys Ala Asp Gly Lys Leu Lys Phe Gln Cys Gly Gln Lys Thr
 130 135 140
 Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu
 145 150 155 160
 Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser
 165 170 175
 Val Thr Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile
 180 185 190
 Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile
 195 200 205
 Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met
 210 215 220

Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp
225 230 235 240

Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys
245 250 255

Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu
260 265 270

Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr
275 280 285

Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu
290 295 300

Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro
305 310 315 320

His Tyr Tyr Gly Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp
325 330 335

Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu
340 345 350

Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp
355 360 365

Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val
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Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly
385 390 395 400

Leu Ala Leu

<210> 7

<211> 323

<212> PRT

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Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
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Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn

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Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys		
35	40	45
Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr		
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Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu		
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		80
Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser		
	85	90
		95
Val Thr Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile		
100	105	110
Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile		
115	120	125
Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met		
130	135	140
Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp		
145	150	155
		160
Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys		
	165	170
		175
Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu		
180	185	190
Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr		
195	200	205
Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu		
210	215	220
Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro		
225	230	235
		240
His Tyr Tyr Gly Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp		
245	250	255
Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu		
260	265	270
Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp		

275	280	285
Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val		
290	295	300
Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly		
305	310	315 320

Leu Ala Leu

<210> 8
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 <213> Homo sapiens

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Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly		
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Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn		
20	25	30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys		
35	40	45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr		
50	55	60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu		
65	70	75 80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu		
85	90	95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp		
100	105	110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val		
115	120	125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu		
130	135	140

<210> 9
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<212> PRT
 <213> Homo sapiens

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Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser
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Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val
 20 25 30

Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly
 35 40 45

Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro
 50 55 60

Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met
 65 70 75 80

Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu
 85 90 95

<210> 10
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 <212> DNA
 <213> Homo sapiens

<400> 10

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 agatctgatg ctcttcagct gggcctgggg aaacataatt actgcaggaa cccagacaac 180
 cggagggcag cctgggtgcta tgtgcagggt ggcctaaagc cgcttggtcca agagtgcag 240
 gtgcatgact gcgcagatgg aaaa 264

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 <211> 141
 <212> DNA
 <213> Homo sapiens

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 cactgtgaaa tagataagtc a 141

<210> 12
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 <212> DNA
 <213> Homo sapiens

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 cactgtgaaa tagataagtc aaaaacctgc tatgagggga atgggtcactt ttaccgagga 180
 aaggccagca ctgacacccat gggccggccc tgccctgccct ggaactctgc cactgtcctt 240
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 tactgcagga acccagacaa ccggaggcga ccctggtgct atgtgcaggt gggcctaaag 360
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 ggggggagaat tcaccacccat cgagaaccag ccctggtttg cgcccatcta caggaggcac 540
 cgggggggct ctgtcaccta cgtgtgtgga ggcagcctca tcagcccttg ctgggtgatc 600
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 <213> Homo sapiens

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 cactgtgaaa tagataagtc aaaaacctgc tatgagggga atgggtcactt ttaccgagga 180
 aaggccagca ctgacacccat gggccggccc tgccctgccct ggaactctgc cactgtcctt 240
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<212> DNA

<213> Homo sapiens

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ccttgctggg tgatcagcgc cacacactgc ttcattgatt acccaaagaa ggaggactac 240
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<211> 1212

<212> DNA

<213> Homo sapiens

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aaggccagca ctgacaccat gggccggccc tgcttgcctt ggaactctgc cactgtcctt 240
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 <212> DNA
 <213> Homo sapiens

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 ggccaaaaga ctctgaggcc ccgctttaag attattgggg gagaattcac caccatcgag 240
 aaccagccct gggttgccgc catctacagg aggcaccggg ggggctctgt cacctacgtg 300
 tgtggaggca gcctcatcag cccttgctgg gtgatcagcg ccacacactg cttcattgat 360
 taccaaaaga aggaggacta catcgtctac ctgggtcgct caaggcttaa ctccaacacg 420
 caaggggaga tgaagtttga ggtggaaaac ctcatcctac acaaggacta cagcgctgac 480
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 tacacgagag tctcacactt cttaccctgg atccgcagtc acaccaagga agagaatggc 960
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 <213> Homo sapiens

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 cactgtgaaa tagataagtc aaaaacctgc tatgagggga atggctactt ttaccgagga 180
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 tactgcagga acccagacaa ccggaggcga ccctgggtgt atgtgcaggt gggcctaaag 360
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 ccagaagaa 429

<210> 18
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<400> 18

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 agatctgatg ctcttcagct gggcctgggg aaacataatt actgcaggaa cccagacaac 180
 cggaggcgac cctgggtgcta tgtgcaggtg ggcctaaagc cgcttgtcca agagtgcatt 240
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